caBIO Wiki Home Page

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At a Glance Details

- Version Number and Release Date: 4.3.2 November, 2012
- Primary audience: Biomedical Informaticians
- Grid Enabled? Yes
- Compatibility Level: Silver
- Installation Level: Intermediate - technical assistance may be required, download may require supporting infrastructure or software
- System Requirements: Refer to caBIO 4.3.2 Technical Guide

caBIO Retirement
The NCI-hosted instance of the Cancer Bioinformatics Infrastructure Objects (caBIO) was retired in November 2013. The scope of this retirement included all caBIO Application Programming Interfaces (APIs), as well as the caBIO Home Page and Portlet. Teams with applications dependent on the NCI-hosted instance of caBIO should migrate to alternate sources of annotations. Please note that a full listing of the data provided through caBIO is available on this wiki. Information and examples on how to transition from caBIO to other data services is available on the caBIO Transition Wiki.

For users that want to install and host their own instance of caBIO, the caBIO software is available on the NCIP caBIO GitHub site. A dump of the caBIO database is available on the NCIP ftp site.

Please direct any questions about caBIO retirement to NCI CBIIT Application Support, ncicbiit@mail.nih.gov.

Tool Overview

Conducting biomedical research requires access to experimental data, as well as associated molecular annotations. Annotations providing detailed information on the molecular origin, biological process, and genetic alterations can provide important insight on experimental outcomes. caBIO (cancer Bioinformatics Infrastructure Objects) is a robust resource for accessing molecular annotations from curated data sources in an integrated view in support of knowledge discovery.

The caBIO domain model and architecture is an ongoing effort to model the rapidly-changing genomics and proteomics domain and to integrate data from numerous sources providing a holistic view of the human and mouse genomes. The entities that concern the Central Dogma of Molecular Biology are the core of the model. The integration of genome annotations with clinical trials, pathway, and literature associations allows researchers to discover associations in the data that were previously unseen in the separate datasets thereby enhancing cancer research and drug design. In caBIO, information is modeled as close to the corresponding biological entities as possible to enable better usability for researchers and application developers alike.

Data for the classes come from a variety of sources, including CGAP, Unigene, the Cancer Gene Index (CGI) project, the Pathway Interaction Database (PID), as well as a number of array manufacturers (for microarray annotations). Given the dynamic nature of this information, the data in caBIO is updated semi-monthly through a series of ETL (Extract, Transform and Load) processes.

Access to this data is provided through a variety of interfaces, including a remote Java API; web services (SOAP and REST API); grid data services available on caGrid; and graphical user interfaces (GUIs) including a caBIO web page and caBIO Portlet available through the caGrid Portal. GUI tools allow researchers to perform a Google ™-like FreestyleLM search that provides end-users with a simple interface to readily browse the contents of the repository. Template-based searches are also available via the caBIO Portlet, allowing researchers to execute common queries based on pre-defined templates.

Installation and Downloads

Downloads for caBIO are available as listed here. The caBIO Software License applies.

The caBIO download provides open source licensing information and access to the caBIO source code, web services, Java client.jar files, programming interfaces, use cases and documentation. Contact Application Support to obtain the latest caBIO schema, database distribution and instructions for installing the database. caBIO is populated with data from many sources. For more information, refer to caBIO Data Sources.

There is also a caBIO GitHub Repository

Sign up for this listserv to receive updates about this tool.

Primary Distribution

The primary distribution contains the client jar files and demonstration programs. The client jar files are a set of Java archive files that define all of the caBIO domain objects, as well as the API classes required to issue queries to the caBIO server.

Java Client - cabio432_java_client.zip

WS Client - cabio432_ws_client.zip

caBIO 4.3.2 Release Notes

caBIO Bundle Javadocs - cabio432_javadocs.zip

Source Code/Server Distribution

The caBIO 4.3.2 source code/server distribution contains the full source code, a deployable .war file, an example JBoss oracle-ds.xml and the caBIO UML models in Enterprise Architect EAP file format.

Source/Server Distribution - cabio432_source.zip

caBIO Source/Server Readme - cabio432_source_readme.txt

Archives

Files from caBIO versions 4.3, 4.2, 4.1, 4.0, 3.2.1, 3.1, 3.0.1.4, 3.0.1.3, 3.0.1, 2.1.3, 2.0.1, 1.2.1, 1.1.1, 1.1 and 1.0 are available for download from the caBIO download archive.

Forum and Support

- Application Support: Telephone: 301-451-4384 or toll free: 888-478-4423; Email
- ICR Workspace Coordinator: Mervi Heiskanen (email)
- caBIO users Listserv - Sign up for tool updates.
- caBIO (API) Users Mail List
- caBIO Developers Mail List (extending the API, adding data sources, enhancing source code)
- caBIO GForge Archive
- caBIO Python API GForge Archive
- caBIO Trackers
- caBIO REST API with Ajax
- caCORE .NET GForge Archive
- caCORE API GForge Archive
- caCORE Perl API GForge Archive

Presentations, Demos and Other Materials

- caBIO Demonstration Site

Documentation and Training

- caBIO Documentation
- caBIO Releases
- caBIO Data Sources
- caBIO FAQ

Related Tools

- geWorkbench
- Pathway Interaction Database(PID)
- Protein Information Resource (PIR)

Collaboration Opportunities

caBIO enables collaboration opportunities through an open development initiative that allows for the contribution of caBIO expanded capabilities. The following caBIO projects are made available through collaborative development efforts:

- caCORE Perl API - Perl API for caBIO services
- pyCaBIO - Python API for caBIO services
- caBIO REST API with Ajax - Example use of AJAX applied to the caBIO REST API
- caBIO .NET API - .NET Project site

If you are interested in participating in collaboration activities, contact Application Support.